

GenCore version 5.1.9  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: July 11, 2006, 17:21:18 ; Search time 30.5853 Seconds  
(without alignments)  
3284.476 Million cell updates/sec

Title: US-10-646-950-6  
Perfect score: 645  
Sequence: 1 cattattagccagatgaatt.....gagagacttcagagctttgaa 362

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 5699196

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame\_n2p,model -DEV=xlp  
-Q=/absw/ABSSWEB\_spool/US10646950/runat\_11072006\_111734\_6250/app\_query.fasta\_1  
-DB=UniProt -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p  
-USER=US10646950\_ECGN\_1\_1\_762\_@runat\_11072006\_111734\_6250 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt\_7.2:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	567	87.9	475	1	FACE1_HUMAN	O75844 homo sapien
2	558	86.5	475	1	FACE1_MOUSE	Q80w54 mus musculu
3	554	85.9	493	2	Q5R6Y6_PONPY	Q5R6Y6 pongo pygma
4	533	82.6	465	2	Q640V5_XENLA	Q640V5 xenopus lae
5	510	79.1	468	2	Q802Z1_BRARE	Q802Z1 brachydanio
6	509	78.9	485	2	Q4RMB6_TETNG	Q4RMB6 tetradon n
7	317.5	49.2	126	2	Q5BKK4_SCHJA	Q5BKK4 schistosoma
8	304.5	47.2	472	2	Q3Y6B8_TAESO	Q3Y6B8 taenia soli
9	296.5	46.0	451	2	Q9V7W7_DROME	Q9V7W7 drosophila
10	271.5	42.1	394	2	Q5TSY1_ANOGA	Q5TSY1 anopheles g
11	271.5	42.1	453	2	Q7QA21_ANOGA	Q7QA21 anopheles g
12	243	37.7	425	2	Q6EPN8_ORYSA	Q6EPN8 oryza sativ
13	242.5	37.6	456	2	Q2JGJ7_ASIPOR	Q2JGJ7 aspergillus
14	240.5	37.3	460	2	Q5SUG3_CRYNE	Q5SUG3 cryptococcu
15	240.5	37.3	460	2	Q5KHY1_CRYNE	Q5KHY1 cryptococcu

16	237	36.7	424	2	Q8RX88_ARATH	Q8rx88 arabidopsis
17	237	36.7	424	2	Q93ZV9_ARATH	Q93zv9 arabidopsis
18	236.5	36.7	479	2	Q4WP06_ASPEU	Q4wp06 aspergillus
19	234.5	36.4	456	2	Q7S178_EMENI	Q7s178 emericella
20	233	36.1	424	2	Q94F88_ARATH	Q94f88 arabidopsis
21	231.5	35.9	442	2	Q7RVV7_NEUCR	Q7rvv7 neurospora
22	231.5	35.9	446	2	Q6IMD9_DEBHA	Q6imd9 debaryomyces
23	231.5	35.9	462	2	Q9C2C0_NEUCR	Q9c2c0 neurospora
24	229.5	35.6	867	2	Q4IA57_GIBBE	Q4ia57 gibberella
25	223.5	34.7	456	2	Q59UR6_CANAL	Q59ur6 candida alb
26	223.5	34.7	456	2	Q8IHA2_DROME	Q8iha2 drosophila
27	220.5	34.2	447	2	Q9V7W6_DROME	Q9v7w6 drosophila
28	217.5	33.7	453	2	Q56D07_PABNR	Q56d07 paracoccidi
29	213	33.0	459	2	Q9M139_ARATH	Q9m139 arabidopsis
30	211.5	32.8	442	2	Q61XW2_CAENR	Q61xw2 caenorhabdi
31	204.5	31.7	442	2	Q9XVFS_CAENR	Q9xvfe caenorhabdi
32	190.5	29.5	453	1	STE24_YEAST	P47154 saccharomyc
33	189.5	29.4	474	1	STE24_SCHPO	Q10071 schizosacch
34	185	28.7	419	2	Q967X5_PHYPO	Q967x5 physarum po
35	176.5	27.4	456	2	Q6CR94_KLULA	Q6cr94 kluyveromyc
36	174	27.0	426	2	Q54FH7_DICTDI	Q54fh7 dictyosteli
37	173.5	26.9	456	2	Q9V7W5_DROME	Q9v7w5 drosophila
38	169.5	26.3	444	2	Q4N3R0_THIEPA	Q4n3r0 theileria p
39	167.5	26.0	438	2	Q4UFQ9_THIEAN	Q4ufq9 theileria a
40	166.5	25.8	316	2	Q04602_ARATH	Q04602 arabidopsis
41	161.5	25.0	460	2	Q6FQ89_CANGA	Q6fq89 candida gla
42	156.5	24.3	422	2	Q3AS21_CHLCH	Q3as21 chlorobium
43	156.5	24.3	427	2	Q38E89_9TRYP	Q38e89 trypanosoma
44	156.5	24.3	453	2	Q2LYG7_9DELT	Q2lyg7 syntrophus
45	153	23.7	410	2	Q3XRV0_9PROT	Q3xrv0 magnetococc

# ALIGNMENTS

## RESULT 1

### FACE1\_HUMAN

ID FACE1\_HUMAN STANDARD; PRT; 475 AA.  
AC O75844; Q8NDZ8; Q9UBQ2;  
DT 15-JUL-1999, integrated into UniProtKB/Swiss-Prot.  
DT 27-APR-2001, sequence version 2.  
DT 07-FEB-2006, entry version 50.  
DE CAAX prenyl protease 1 homolog (EC 3.4.24.84) (Prenyl protein-specific  
DE endoprotease 1) (Farnesylated proteins-converting enzyme 1) (FACE-1)  
DE (Zinc metalloproteinase Ste24 homolog).  
GN Name=ZMPSTE24; Synonyms=FACE1, STE24;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OK NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Brain;  
RX MEDLINE=99177429; PubMed=10076063; DOI=10.1016/S0304-4165(98)00170-6;  
RA Kumagai H., Kawamura Y., Yanagisawa K., Komano H.;  
RT "Identification of a human cDNA encoding a novel protein structurally  
RT related to the yeast membrane-associated metalloprotease, Ste24p.";  
RL Biochim. Biophys. Acta 1426:468-474(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=B-cell, and Fetal brain;  
RX MEDLINE=98365461; PubMed=9700155; DOI=10.1083/jcb.142.3.635;  
RA Tam A., Nouvet F.J., Fujimura-Kamada K., Slunt H., Sisodia S.S.,  
RA Michaelis S.;  
RT "Dual roles for Ste24p in yeast a-factor maturation: NH2-terminal  
RT proteolysis and COOH-terminal CAAX processing.";  
RL J. Cell Biol. 142:635-649(1998).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Ovary;  
RX MEDLINE=99303558; PubMed=10373325; DOI=10.1006/geno.1999.5834;

RA Freije J.M.P., Blay P., Pendas A.M., Cadinanos J., Crespo P.,  
 Lopez-Otin C.;  
 RT \*Identification and chromosomal location of two human genes encoding  
 RT enzymes potentially involved in proteolytic maturation of farnesylated  
 RT proteins.\*;  
 RL Genomics 58:270-280(1999).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RG Human chromosome 1 international sequencing consortium;  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Testis;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klauwetter R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bonak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT \*Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.\*;  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RP VARIANT MADB ARG-340.  
 RX MEDLINE=22793839; PubMed=12913070; DOI=10.1093/hmg/dmg213;  
 RA Agarwal A.K., Fryns J.-P., Auchus R.J., Garg A.;  
 RT \*Zinc metalloproteinase, ZMPSTE24, is mutated in mandibuloacral  
 RT dysplasia.\*;  
 RL Hum. Mol. Genet. 12:1995-2001(2003).  
 CC -!- FUNCTION: Proteolytically removes the C-terminal three residues of  
 CC farnesylated proteins. Acts on lamin A/C.  
 CC -!- CATALYTIC ACTIVITY: The peptide bond hydrolyzed can be designated  
 CC -C-[A-A-X in which C is an S-isoprenylated cysteine residue, A is  
 CC usually aliphatic and X is the C-terminal residue of the substrate  
 CC protein, and may be any of several amino acids.  
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
 CC reticulum and possibly also the Golgi compartment.  
 CC -!- TISSUE SPECIFICITY: Widely expressed. High levels in kidney,  
 CC prostate, testis and ovary.  
 CC -!- DISEASE: Defects in ZMPSTE24 are the cause of mandibuloacral  
 CC dysplasia with type B lipodystrophy (MADB) [MIM:608612].  
 CC Mandibuloacral dysplasia (MAD) is a rare autosomal recessive  
 CC disorder characterized by mandibular and clavicular hypoplasia,  
 CC acroosteolysis, delayed closure of the cranial suture, joint  
 CC contractures, and types A or B patterns of lipodystrophy. Type B  
 CC lipodystrophy observed in MADB, is characterized by generalized  
 CC fat loss.  
 CC -!- SIMILARITY: Belongs to the peptidase M48A family.  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 DR EMBL; AB016068; BAA33727.1; -; mRNA.  
 DR EMBL; AF064867; AAC68866.1; -; mRNA.  
 DR EMBL; Y13834; CAB46277.1; -; mRNA.  
 DR EMBL; AL050341; CAB81610.1; -; Genomic\_DNA.  
 DR EMBL; BC037283; AAH37283.1; -; mRNA.  
 DR MEROPS; M48.003; -.

DR Ensembl; ENSG00000084073; Homo sapiens.  
 DR HGNC; HGNC:12877; ZMPSTE24.  
 DR MIM; 606480; gene.  
 DR MIM; 608612; phenotype.  
 DR GO; GO:0005235; F:metalloexopeptidase activity; TAS.  
 DR GO; GO:0006908; P:proteolysis and peptidolysis; TAS.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro; IPR001915; Peptidase\_M48.  
 DR Pfam; PF01435; Peptidase\_M48; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; FALSE\_NEG.  
 KW Disease mutation; Endoplasmic reticulum; Golgi stack; Hydrolase;  
 KW Membrane; Metal-binding; Metalloprotease; Protease; Transmembrane;  
 KW Zinc.  
 FT CHAIN 1 475 CAAX prenyl protease 1 homolog.  
 FT /FTID-PRO\_0000138844.  
 FT TRANSMEM 19 39 Potential.  
 FT TRANSMEM 82 102 Potential.  
 FT TRANSMEM 124 144 Potential.  
 FT TRANSMEM 171 191 Potential.  
 FT TRANSMEM 196 216 Potential.  
 FT TRANSMEM 348 368 Potential.  
 FT TRANSMEM 383 405 Potential.  
 FT ACT\_SITE 336 336 By similarity.  
 FT ACT\_SITE 419 419 Proton donor (By similarity).  
 FT METAL 335 335 Zinc (catalytic) (By similarity).  
 FT METAL 339 339 Zinc (catalytic) (By similarity).  
 FT METAL 415 415 Zinc (catalytic) (By similarity).  
 FT VARIANT 340 340 W -> R (in MADB).  
 FT /FTID-VAR\_019308.  
 FT CONFLICT 16 16 E -> K (in Ref. 1).  
 FT CONFLICT 137 137 T -> A (in Ref. 5; AAH37283).  
 SQ SEQUENCE 475 AA; 54813 MW; 6C49179DEB0C8F7F CRC64;

Alignment Scores:  
 Pred. No.: 9.88e-64 Length: 475  
 Score: 567.00 Matches: 115  
 Percent Similarity: 95.8% Conservative: 0  
 Best Local Similarity: 95.8% Mismatches: 5  
 Query Match: 87.9% Indels: 1  
 DB: 1 Gaps: 0

US-10-646-950-6 (1-362) x FACEL\_HUMAN (1-475)

```

Qy      2 ATTATTAGCCAGATGAATCTCTTCCTGTGTTTTTTTTTATTGCTGTATTAAATGGTCGA 61
      |||
Db      350 IleIleSerGlnMetAsnSerPheLeuCysPhePheLeuPheAlaValIleGlyArg 369

Qy      62 AAGGAGCTTTTGTGCATTGGTTTTTATGNTAGCCAACCCACTNTTATTGGACTATTG 121
      |||
Db      370 LysGluLeuPheAlaAlaPheGlyPheTyrAspSerGlnProThrLeuIleGlyLeuLeu 389

Qy      122 NTCATCTTCCAGTTTATTTTTTTCACCTTACAATGNGGTTCTTCTTTTGGCTAACAGTC 181
      |||
Db      390 IleIlePheGlnPheIlePheSerProTyrAsnGluValLeuSerPheCysLeuThrVal 409

Qy      182 CTAAGCCGCGAGATTGAGTTTCAAGGTGATGCATT-GCCAAAGAACTTGGGAAGGCTAAA 240
      |||
Db      410 LeuSerArgArgPheGluPheGlnAlaAspAlaPheAlaLysLysLeuGlyLysAlaLys 429

Qy      241 GACITATATCTGCTTTAATCAAACTTAACAAGATAACTTGGGATTCCCTGTTTCTGAC 300
      |||
Db      430 AspLeuTyrSerAlaLeuIleLysLeuAsnLysAspAsnLeuGlyPheProValSerAsp 449

Qy      301 TGGTTGTTCTCAATGTGGCATATTCTCATCTCCACTGCTAGAGAGACTTCAAGCTTTG 360
      |||
Db      450 TrpLeuPheSerMetTrpHisTyrSerHisProProLeuLeuGlnArgLeuGlnAlaLeu 469

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